

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Articles selected by Faculty of **1000**: archaeal adaptation to cold; human chromosome 7 sequence; comparative protein-structure modeling; new algorithm for sequence alignment; expression profiling human mast cells

ArticleInfo		
ArticleID	:	3470
ArticleDOI	:	10.1186/gb-2003-4-9-338
ArticleCitationID	:	338
ArticleSequenceNumber	:	18
ArticleCategory	:	Paper report
ArticleFirstPage	:	1
ArticleLastPage	:	3
ArticleHistory	:	RegistrationDate : 2003-8-7 OnlineDate : 2003-8-7

ArticleCopyright	:	BioMed Central Ltd2003
ArticleGrants	:	
ArticleContext	:	130594499

## The Author(s)

### Summary

A selection of evaluations from Faculty of 1000 covering genomic analysis of cold-adapted methanogenic archaea, the sequence of human chromosome 7, comparative protein-structure modeling, a new algorithm for multiple sequence alignment and expression profiling human mast cells.

## Archaeal adaptation to cold

**Mechanisms of thermal adaptation revealed from the genomes of the antarctic archaea *Methanogenium frigidum* and *Methanococcoides burtonii*** . Saunders NF, Thomas T, Curmi PM, Mattick JS, Kuczek E, Slade R, Davis J, Franzmann PD, Boone D, Rusterholtz K, *et al.* *Genome Res* 2003, **13**:1580-1588.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-9-338.asp#Saunders>

## Human chromosome 7 sequence

**The DNA sequence of human chromosome 7.** Hillier LW, Fulton RS, Waterston RH, Wilson RK and colleagues. *Nature* 2003, **424**:157-164.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-9-338.asp#Hillier>

## Comparative protein-structure modeling

**Comparative protein structure modeling by iterative alignment, model building and model assessment.** John B, Sali A. *Nucleic Acids Res* 2003, **31**:3982-3892.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-9-338.asp#John>

## New algorithm for sequence alignment

**SATCHMO: sequence alignment and tree construction using hidden Markov models.** Edgar RC, Sjölander K. *Bioinformatics* 2003, **19**:1404-1411.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-9-338.asp#Edgar>

## Expression profiling human mast cells

**Identification of specific gene expression profile in human mast cells via Toll-like receptor 4 and Fc{epsilon}RI.** Okumura S, Kashiwakura JI, Tomita H, Matsumoto K, Nakajima T, Saito H, Okayama Y. *Blood* 2003, Jul 10.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-9-338.asp#Okumura>